==========

Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2009; month=5; day=22; hr=12; min=43; sec=5; ms=375;]

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Validated By CRFValidator v 1.0.3

Application No: 10594258 Version No: 1.0

Input Set:

Output Set:

Started: 2009-05-08 19:38:51.479
Finished: 2009-05-08 19:38:53.432
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 953 ms
Total Warnings: 12
Total Errors: 12
No. of SeqIDs Defined: 16
Actual SeqID Count: 16

Error code		Error Description
W	213	Artificial or Unknown found in <213> in SEQ ID (5)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (5)
W	213	Artificial or Unknown found in <213> in SEQ ID (6)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (6)
W	213	Artificial or Unknown found in <213> in SEQ ID (7)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (7)
W	213	Artificial or Unknown found in <213> in SEQ ID (8)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (8)
W	213	Artificial or Unknown found in <213> in SEQ ID (9)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (9)
W	213	Artificial or Unknown found in <213> in SEQ ID (10)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (10)
W	213	Artificial or Unknown found in <213> in SEQ ID (11)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (11)
W	213	Artificial or Unknown found in <213> in SEQ ID (12)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (12)

Input Set:

Output Set:

Started: 2009-05-08 19:38:51.479
Finished: 2009-05-08 19:38:53.432
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 953 ms
Total Warnings: 12
Total Errors: 12
No. of SeqIDs Defined: 16
Actual SeqID Count: 16

Error code		Error Description
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E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (13)
W	213	Artificial or Unknown found in <213> in SEQ ID (14)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (14)
W	213	Artificial or Unknown found in <213> in SEQ ID (15)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (15)
W	213	Artificial or Unknown found in <213> in SEQ ID (16)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (16)

SEQUENCE LISTING

<110> Wageningen Centre for Food Sciences

<120> Novel mannose-specific adhesins and their use

<130> P212925EP

<140> 10594258
<141> 2009-05-08

<150> EP04075945.8
<151> 2004-03-23

<160> 16

<170> PatentIn version 3.1

<210> 1

<211> 1010

<212> PRT

<213> Lactobacillus plantarum

<400> 1

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Leu Gly Val Gly Thr Val Thr Met Thr Arg Ala Ala Ala Ala Asp Ser
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Glu Val Thr Asn Asp Ser Ala Ser Gln His Val Thr Ser Ile Ser Thr
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    50                  55                  60

Asp Ala Ser Lys Asn Gln His Thr Ser Ser Asn Val Ile Leu Thr Asn
65                  70                  75                  80

Asp Asp Lys Ser Val Ser Ala Ser Ile Asn Gln Asp Ala Ser Ala Ser
                85                  90                  95

Val Val Asn Lys Ala Val Ser Ala Thr Ser Gln Glu Asn Ser Ser Val
            100                 105                 110

Gln Asn Thr Ser Gln Ala Thr Ser Thr Ser Lys Gln Glu Ser Ser Ser
        115                 120                 125

Thr Lys Asn Thr Ser Gln Thr Thr Ser Thr Ser Asn Gln Glu Ala Asn
    130                 135                 140

Ser Ala Lys Ser Ile Asn Gln Thr Thr Arg Thr Ser Lys Gln Glu Ser
145                 150                 155                 160

Ser Ser Thr Lys Asn Thr Ser Gln Thr Thr Ser Thr Ser Asn Gln Glu
                165                 170                 175

Ala Asn Ser Ala Lys Ser Ile Asn Gln Thr Thr Arg Thr Ser Asn Gln
            180                 185                 190

Glu Ser Ser Ser Ala Lys Asn Thr Ser Gln Thr Thr Ser Thr Ser Ser
        195                 200                 205

Arg Lys Ile Asn Ser Thr Lys Ser Gln Ala Gln Ser Leu Thr Ile Thr
    210                 215                 220

Thr Thr Gly Lys Ala Val Arg Ala Thr Ser Thr Ser Val Lys Lys Tyr
225                 230                 235                 240

Ser Thr Lys Thr Lys Val Ser Tyr Ser Thr Leu Leu Gln Gln Leu Arg
                245                 250                 255

Thr Ser Lys Ala Leu Ile Ser Asp Glu Ala Ala Leu Thr His Val Asp
            260                 265                 270

Lys Asp Asn Phe Leu Lys Tyr Phe Ser Leu Asn Gly Ser Ala Thr Tyr
        275                 280                 285
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Asp Ala Lys Thr Gly Ile Val Thr Ile Thr Pro Asn Gln Asn Asn Gln
    290                 295                 300

Val Gly Asn Phe Ser Leu Thr Ser Lys Ile Asp Met Asn Lys Ser Phe
305                 310                 315                 320

Thr Leu Thr Gly Gln Val Asn Leu Gly Ser Asn Pro Asn Gly Ala Asp
                325                 330                 335

Gly Ile Gly Phe Ala Phe His Ser Gly Asn Thr Thr Asp Val Gly Asn
            340                 345                 350

Ala Gly Gly Asn Leu Gly Ile Gly Gly Leu Gln Asp Ala Ile Gly Phe
        355                 360                 365

Lys Leu Asp Thr Trp Phe Asn Ser Tyr Gln Ala Pro Ser Ser Asp Lys
    370                 375                 380

Asn Gly Ser Glu Ile Ser Ser Thr Asn Ser Asn Gly Phe Gly Trp Asn
385                 390                 395                 400

Gly Asp Ser Ala Asn Ala Pro Tyr Gly Thr Phe Val Lys Thr Ser Asn
                405                 410                 415

Gln Glu Ile Ser Thr Ala Asn Gly Ser Lys Val Gln Arg Trp Trp Ala
            420                 425                 430

Gln Asp Thr Gly Glu Ser Gln Ala Leu Ser Lys Ala Asp Ile Asp Gly
        435                 440                 445

Asn Phe His Asp Phe Val Val Asn Tyr Asp Gly Ala Thr Arg Thr Leu
    450                 455                 460

Thr Val Ser Tyr Thr Gln Ala Ser Gly Lys Val Leu Thr Trp Lys Thr
465                 470                 475                 480

Thr Val Asp Ser Ser Tyr Gln Ala Met Ala Met Val Val Ser Ala Ser
                485                 490                 495

Thr Gly Ala Ala Lys Asn Leu Gln Gln Phe Lys Leu Thr Ser Phe Asp
            500                 505                 510
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Phe Gln Glu Ala Ala Thr Val Asn Val Lys Tyr Val Asp Thr Thr Gly
        515                 520                 525

His Gln Leu Ala Gln Gly Thr Ala Asn Tyr Pro Asp Gly Ala Tyr Val
    530                 535                 540

Asn Gly Arg Tyr Thr Thr Lys Gln Leu Ile Ile Pro Asn Tyr Arg Phe
545                 550                 555                 560

Ile Lys Met Asp Asp Gly Ser Val Thr Gly Thr Lys Ser Leu Asp Ala
                565                 570                 575

Asn Gly Thr Leu Ile Gln Ser Gly Asp Asn Gly Thr Val Ile Tyr Val
            580                 585                 590

Tyr Val Pro Glu Tyr Met Ala Ile Val Lys Thr Val Asn Glu Thr Ile
        595                 600                 605

Asn Tyr Val Asp Glu Asn Gly His Ala Leu Thr Thr Ser Tyr Thr Ala
    610                 615                 620

Asn Pro Ile His Ile Leu Thr Val Thr Asn Pro Val Asp Gly Thr Thr
625                 630                 635                 640

Thr Thr Tyr Tyr Ser Thr Ile Thr Thr Ser Ile Glu Leu Asp Ala Thr
                645                 650                 655

Thr Gly Arg Pro Val Asp Ser Gly Trp Val Leu Gly Asn Ser Gln Asp
            660                 665                 670

Phe Asp Ala Val Thr Asn Pro Gln Ile Lys Gly Tyr Thr Val Thr Ser
        675                 680                 685

Thr Asp Ala Pro Asn Ser Asp Leu Gln His Val Ser Ala Gln Thr Val
    690                 695                 700

Thr Gly Asp Ser Gly Asp Leu Glu Phe Thr Val Val Tyr Thr Lys Asn
705                 710                 715                 720

Ala Pro Ile Val Thr Thr Glu Ser Lys Thr Val Asn Glu Thr Ile His
                725                 730                 735
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Tyr Val Tyr Thr Asp Gly Thr Thr Ala His Asp Asp Tyr Val Ala Gln
            740                 745                 750

Pro Ile Thr Phe Thr Arg Thr Val Phe Thr Asp Ala Val Thr Gly Glu
        755                 760                 765

Lys Thr Tyr Gly Gly Trp Ser Ala Ala Gln Gln Phe Ala Ala Val Asp
    770                 775                 780

Ser Pro Ala Ile Lys Gly Tyr Thr Pro Asp Gln Ser Lys Ile Ser Thr
785                 790                 795                 800

Gln Thr Val Thr Gly Asp Ser Ser Asp Leu Glu Phe Thr Ile Val Tyr
                805                 810                 815

Thr Lys Asn Ala Pro Thr Val Thr Thr Glu Ser Lys Thr Val Asn Glu
            820                 825                 830

Thr Ile His Tyr Val Tyr Thr Asp Gly Thr Ile Ala His Asp Asp Tyr
        835                 840                 845

Val Ala Gln Pro Ile Thr Phe Thr Arg Thr Val Ser Thr Asp Ala Val
    850                 855                 860

Thr Gly Glu Lys Thr Tyr Gly Gly Trp Ser Ala Ala Gln Gln Phe Ala
865                 870                 875                 880

Ala Val Asp Ser Pro Ala Ile Lys Gly Tyr Thr Pro Asp Gln Ser Lys
                885                 890                 895

Ile Ser Thr Gln Thr Val Thr Gly Asp Ser Ser Asp Leu Glu Phe Thr
            900                 905                 910

Val Val Tyr Lys Ala Asp Ser Thr Ser Thr Lys Pro Val Lys Pro Glu
        915                 920                 925

Gln Pro Thr Ile Pro Thr Thr Pro Thr Glu Pro Val Lys Pro Gly Gln
    930                 935                 940

Leu Thr Thr Pro Ala Lys Pro Asp Gln Pro Met Thr Ser Asp Lys Ser
945                 950                 955                 960

Val Gln Thr Ile Thr Ile Lys Phe Val Gly Gln Arg Leu Pro Gln Thr
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965 970 975

Asn Glu Thr Asp Gln Gln His Met Thr Leu Ser Gly Leu Leu Leu Leu
980 985 990

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Lys Glu
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<213> Lactobacillus plantarum

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acacgggccg ccgcagcaga ttccgaagtg acgaacgatt cagcatctca acatgtgacg 180

agcatctcta ctgatgcgtc taaaaatcag catacgtcta gtaatgtgat tcttacaaat 240

gatgataaaa gtgttagtgc atcaattaat caagacgcta gcgcgagtgt tgtcaataag 300

gcggtcagcg caactagcca agaaaatagt agcgttcaaa atactagtca ggcaaccagt 360

acaagcaaac aagaatccag tagtacgaaa aatactagtc agacaaccag tacaagcaat 420

caagaagcta acagtgccaa gagtattaat caaacgaccc gtacaagcaa acaagaatcc 480

agtagtacga aaaatactag tcagacaacc agtacaagca atcaagaagc taacagtgcc 540

aagagtatta atcaaacgac ccgtacaagc aatcaagaat ccagtagtgc gaaaaatact 600

agtcagacaa ccagtacaag tagtcggaag attaatagca ctaaaagcca agcccaatca 660

ttaacaatta cgactacggg caaagcggtt cgtgctacct cgactagtgt taaaaagtac 720

tccaccaaga caaaagtgtc atatagcaca ttgttacagc agcttcgtac aagtaaagcg 780

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caaaataatc aagttggtaa tttttcatta accagtaaga ttgatatgaa taaaagcttt 960

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gcttttcaca gtggcaatac aactgacgtg ggaaatgctg gtggtaattt aggtattggt 1080

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ggagcgtatg tcaatggtcg gtacaccact aaacaattaa taattcccaa ttatagattt 1680

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<212> PRT

<213> Lactobacillus plantarum

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Ile Lys Ser Trp Leu Val Ser Ser Tyr Ser Pro Thr Val Thr Ala Lys
35 40 45

Thr Val Lys Gln Asn Thr Lys Lys Lys Ser Asp Phe Asn Phe Ser Lys
50 55 60

Val Lys Ser Leu Asp Phe Gln Thr Val Ala Lys Ala Arg Met Asn Lys
65 70 75 80

Asn Ala Ile Asn Val Ile Gly Ser Ile Ala Ile Pro Ser Val Asp Leu
85 90 95

Tyr Leu Pro Ile Gly Asn Gly Val Ser Asn Glu Thr Leu Ala Leu Ala
100 105 110

Ala Gly Thr Met Lys Ala Asn Gln Lys Met Gly Gln Gly Asn Tyr Ala
115 120 125

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Leu Ala Gly His His Met Ile Lys His Gly Ala Leu Phe Ser Pro Leu
    130                 135                 140

Tyr Tyr Lys Ser Lys Val Gly Gln Met Ile Tyr Val Ser Asp Ala Lys
145                 150                 155                 160

Lys Ile Tyr Ala Tyr Lys Thr Ser Gln Arg Thr Phe Ile Lys Ala Thr
                165                 170                 175

Asp Val Gln Val Ile Asp Asp Val Pro Gly Gln Lys Leu Ile Thr Leu
            180                 185                 190

Ile Thr Cys Asp Lys Thr Gly Ala Gly Arg Leu Met Ile Arg Gly Lys
        195                 200                 205

Tyr Glu Gln Gln Trp Ser Phe Lys Ser Ala Pro Thr Gln Val Gln Lys
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<212> DNA

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tactcgccga ccgttacggc taagacggtt aagcagaata cgaagaagaa gagcgatttt    180

aacttctcaa aggtcaagtc acttgacttt cagaccgttg ccaaggcccg catgaataag    240

aatgcaatca acgtgattgg ctcgattgcg attccgtccg ttgatttgta cctgccaatc    300

ggtaatggtg tcagcaatga aacgttagca ttggcggctg gcacgatgaa agctaatcag    360

aagatggggc agggtaacta cgcgttggct ggtcaccata tgatcaagca tggtgcacta    420

ttcagtccgt tgtactataa gagcaaggtt ggccaaatga tttatgtgag tgatgccaaa    480
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attgatgatg ttcctggtca gaagctgatt accctaatta cctgtgataa gaccggggcg 600

ggtcgcttaa tgattcgcgg taagtacgaa cagcaatggt cgtttaagtc ggcgccaact 660

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ccattacgat gatgtttccc 20

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